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2-28-01

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/711,724
DATE: 11/29/2000
TIME: 13:33:00

Input Set : A:\Hmv00606.app
Output Set: N:\CRF3\11292000\I711724.raw

ENTERED

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:
6 (i) APPLICANT: Ingham, Phillip W.
7 McMahon, Andrew P.
8 Tabin, Clifford J.
9 Marigo, Valeria
11 (ii) TITLE OF INVENTION: SCREENING ASSAYS FOR HEDGEHOG AGONISTS
12 AND ANTAGONISTS
14 (iii) NUMBER OF SEQUENCES: 48
16 (iv) CORRESPONDENCE ADDRESS:
17 (A) ADDRESSEE: FOLEY, HOAG & ELIOT LLP
18 (B) STREET: One Post Office Square
19 (C) CITY: Boston
20 (D) STATE: MA
21 (E) COUNTRY: USA
22 (F) ZIP: 02109-2170
24 (v) COMPUTER READABLE FORM:
25 (A) MEDIUM TYPE: Floppy disk
26 (B) COMPUTER: IBM PC compatible
27 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
28 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
30 (vi) CURRENT APPLICATION DATA:
C--> 31 (A) APPLICATION NUMBER: US/09/711,724
C--> 32 (B) FILING DATE: 13-Nov-2000
33 (C) CLASSIFICATION:
35 (vii) PRIOR APPLICATION DATA:
36 (A) APPLICATION NUMBER: US 08/460,900
37 (B) FILING DATE: 05-JUN-1995
39 (viii) ATTORNEY/AGENT INFORMATION:
40 (A) NAME: Vincent, Matthew P.
41 (B) REGISTRATION NUMBER: 36,709
42 (C) REFERENCE/DOCKET NUMBER: Hmv-006.06
44 (ix) TELECOMMUNICATION INFORMATION:
45 (A) TELEPHONE: 617-832-1000
46 (B) TELEFAX: 617-832-7000
49 (2) INFORMATION FOR SEQ ID NO: 1:
51 (i) SEQUENCE CHARACTERISTICS:
52 (A) LENGTH: 1277 base pairs
53 (B) TYPE: nucleic acid
54 (C) STRANDEDNESS: both
55 (D) TOPOLOGY: linear
57 (ii) MOLECULE TYPE: cDNA
60 (ix) FEATURE:
61 (A) NAME/KEY: CDS
62 (B) LOCATION: 1..1275
65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
67 ATG GTC GAA ATG CTG CTG TTG ACA AGA ATT CTC TTG GTG GGC TTC ATC 48

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68	Met	Val	Glu	Met	Leu	Leu	Leu	Thr	Arg	Ile	Leu	Leu	Val	Gly	Phe	Ile	
69	1				5					10					15		
71	TGC	GCT	CTT	TTA	GTC	TCC	TCT	GGG	CTG	ACT	TGT	GGA	CCA	GGC	AGG	GGC	96
72	Cys	Ala	Leu	Leu	Val	Ser	Ser	Gly	Leu	Thr	Cys	Gly	Pro	Gly	Arg	Gly	
73					20				25					30			
75	ATG	GGA	AAA	ACG	AGG	CAC	CCC	AAA	AAG	CTG	ACC	CCG	TTA	GCC	TAT	AAG	144
76	Ile	Gly	Lys	Arg	Arg	His	Pro	Lys	Lys	Leu	Thr	Pro	Leu	Ala	Tyr	Lys	
77					35				40					45			
79	CAG	TTT	ATT	CCC	AAT	GTG	GCA	GAG	AAG	ACC	CTA	GGG	GCC	AGT	GGA	AGA	192
80	Gln	Phe	Ile	Pro	Asn	Val	Ala	Glu	Lys	Thr	Leu	Gly	Ala	Ser	Gly	Arg	
81					50				55					60			
83	TAT	GAA	GGG	AAG	ATC	ACA	AGA	AAC	TCC	GAG	AGA	TTT	AAA	GAA	CTA	ACC	240
84	Tyr	Glu	Gly	Lys	Ile	Thr	Arg	Asn	Ser	Glu	Arg	Phe	Lys	Glu	Leu	Thr	
85	65								70					75			
87	CCA	AAT	TAC	AAC	CCT	GAC	ATT	ATT	TTT	AAG	GAT	GAA	GAG	AAC	ACG	GGA	288
88	Pro	Asn	Tyr	Asn	Pro	Asp	Ile	Ile	Phe	Lys	Asp	Glu	Glu	Asn	Thr	Gly	
89					85					90				95			
91	GCT	GAC	AGA	CTG	ATG	ACT	CAG	CGC	TGC	AAG	GAC	AAG	CTG	AAT	GCC	CTG	336
92	Ala	Asp	Arg	Leu	Met	Thr	Gln	Arg	Cys	Lys	Asp	Lys	Leu	Asn	Ala	Leu	
93					100					105				110			
95	GCG	ATC	TCG	GTG	ATG	AAC	CAG	TGG	CCC	GGG	GTG	AAG	CTG	CGG	GTG	ACC	384
96	Ala	Ile	Ser	Val	Met	Asn	Gln	Trp	Pro	Gly	Val	Lys	Leu	Arg	Val	Thr	
97					115				120					125			
99	GAG	GGC	TGG	GAC	GAG	GAT	GGC	CAT	CAC	TCC	GAG	GAA	TCG	CTG	CAC	TAC	432
100	Glu	Gly	Trp	Asp	Glu	Asp	Gly	His	His	Ser	Glu	Glu	Ser	Leu	His	Ile	
101					130				135				140				
103	GAG	GGT	CGC	GCC	GTG	GAC	ATC	ACC	ACG	TCG	GAT	CGG	GAC	CGC	AGC	AAG	480
104	Glu	Gly	Arg	Ala	Val	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Arg	Ser	Lys	
105	145								150				155				
107	TAC	GGA	ATG	CTG	GCC	CGC	CTC	GCC	GTG	GAG	GCC	GGC	TTC	GAC	TGG	GTC	528
108	Tyr	Gly	Met	Leu	Ala	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	
109					165					170				175			
111	TAC	TAC	GAG	TCC	AAG	GCG	CAC	ATC	CAC	TGC	TCC	GTC	AAA	GCA	GAA	AAC	576
112	Tyr	Tyr	Glu	Ser	Lys	Ala	His	Ile	His	Cys	Ser	Val	Lys	Ala	Glu	Asn	
113					180					185				190			
115	TCA	GTG	GCA	GCG	AAA	TCA	GGA	GGC	TGC	TTC	CCT	GGC	TCA	GCC	ACA	GTG	624
116	Ser	Val	Ala	Ala	Lys	Ser	Gly	Gly	Cys	Phe	Pro	Gly	Ser	Ala	Thr	Val	
117					195				200					205			
119	CAC	CTG	GAG	CAT	GGA	GGC	ACC	AAG	CTG	GTG	AAG	GAC	CTC	AGC	CCT	GGG	672
120	His	Leu	Glu	His	Gly	Gly	Thr	Lys	Leu	Val	Lys	Asp	Leu	Ser	Pro	Gly	
121					210				215					220			
123	GAC	CGC	GTG	CTG	GCT	GCT	GAC	GCG	GAC	GGC	CGG	CTG	CTC	TAC	AGT	GAC	720
124	Asp	Arg	Val	Leu	Ala	Ala	Asp	Ala	Asp	Gly	Arg	Leu	Leu	Tyr	Ser	Asp	
125	225								230					235			
127	TTC	CTC	ACC	TTC	CTC	GAC	CGG	ATG	GAC	AGC	TCC	CGA	AAG	CTC	TTC	TAC	768
128	Phe	Leu	Thr	Phe	Leu	Asp	Arg	Met	Asp	Ser	Ser	Arg	Lys	Leu	Phe	Tyr	
129					245					250				255			
131	GTC	ATC	GAG	ACG	CGG	CAG	CCC	CGG	GCC	CGG	CTG	CTA	CTG	ACG	GCG	GCC	816
132	Val	Ile	Glu	Thr	Arg	Gln	Pro	Arg	Ala	Arg	Leu	Leu	Leu	Thr	Ala	Ala	

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133          260          265          270
135 CAC CTG CTC TTT GTG GCC CCC CAG CAC AAC CAG TCG GAG GCC ACA GGC      864
136 His Leu Leu Phe Val Ala Pro Gln His Asn Gln Ser Glu Ala Thr Gly
137          275          280          285
139 TCC ACC AGT GCC CAG GCG CTC TTC GCC AGC AAC GTG AAG CCT GGC CAA      912
140 Ser Thr Ser Gly Gln Ala Leu Phe Ala Ser Asn Val Lys Pro Gly Gln
141          290          295          300
143 CGT GTC TAT GTG CTG GGC GAG GGC GGG CAG CAG CTG CTG CCG GCG TCT      960
144 Arg Val Tyr Val Leu Gly Glu Gly Gly Gln Gln Leu Leu Pro Ala Ser
145 305          310          315
147 GTC CAC AGC GTC TCA TTG CGG GAG GAG GCG TCC GGA GCC TAC GCC CCA      1008
148 Val His Ser Val Ser Leu Arg Glu Glu Ala Ser Gly Ala Tyr Ala Pro
149          325          330          335
151 CTC ACC GCC CAG GGC ACC ATC CTC ATC AAC CGG GTG TTG GCC TCC TGC      1056
152 Leu Thr Ala Gln Gly Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys
153          340          345
155 TAC GCC GTC ATC GAG GAG CAC AGT TGG GCC CAT TGG GCC TTC GCA CCA      1104
156 Tyr Ala Val Ile Glu Glu His Ser Trp Ala His Trp Ala Phe Ala Pro
157          355          360          365
159 TTC CGC TTG GCT CAG GGG CTG CTG GCC GCC CTC TGC CCA GAT GGG GCC      1152
160 Phe Arg Leu Ala Gln Gly Leu Leu Ala Ala Leu Cys Pro Asp Gly Ala
161          370          375          380
163 ATC CCT ACT GCC GCC ACC ACC ACT GGC ATC CAT TGG TAC TCA CGG      1200
164 Ile Pro Thr Ala Ala Thr Thr Thr Gly Ile His Trp Tyr Ser Arg
165 385          390          395
167 CTC CTC TAC CGC ATC GGC AGC TGG GTG CTG GAT GGT GAC GCG CTG CAT      1248
168 Leu Leu Tyr Arg Ile Gly Ser Trp Val Leu Asp Gly Asp Ala Leu His
169          405          410          415
171 CCG CTG GGC ATG GTG GCA CCG GCC AGC TG      1277
172 Pro Leu Gly Met Val Ala Pro Ala Ser
173          420          425
176 (2) INFORMATION FOR SEQ ID NO: 2:
177 (i) SEQUENCE CHARACTERISTICS:
178 (A) LENGTH: 1190 base pairs
179 (B) TYPE: nucleic acid
180 (C) STRANDEDNESS: single
181 (D) TOPOLOGY: linear
182 (ii) MOLECULE TYPE: cDNA
183 (ix) FEATURE:
184 (A) NAME/KEY: CDS
185 (B) LOCATION: 1..1188
186 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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194 ATG GCT CTG CCG GCC AGT CTG TTG CCC CTG TGC TGC TTG GCA CTC TTG      48
195 Met Ala Leu Pro Ala Ser Leu Leu Pro Leu Cys Cys Leu Ala Leu Leu
196 1          5          10          15
198 GCA CTA TCT GCC CAG AGC TGC GGC CCG GGC CGA GGA CCG GTT GGC CGG      96
199 Ala Leu Ser Ala Gln Ser Cys Gly Pro Gly Arg Gly Pro Val Gly Arg
200          20          25          30
202 CGG CGT TAT GTG CGC AAG CAA CTT GTG CCT CTG CTA TAC AAG CAG TTT      144

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203	Arg	Arg	Tyr	Val	Arg	Lys	Gln	Leu	Val	Pro	Leu	Leu	Tyr	Lys	Gln	Phe	
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206	GTG	CCC	AGT	ARG	CCC	GAG	CGG	ACC	CTG	GGC	GCG	AGT	GGG	CCA	GCG	GAG	
207	Val	Pro	Ser	Met	Pro	Glu	Arg	Thr	Leu	Gly	Ala	Ser	Gly	Pro	Ala	Glu	
208		50				55						60					240
210	GGG	AGG	GTA	ACA	AGG	GGG	TCG	GAG	CGC	TTC	CGG	GAC	CTC	GTA	CCC	AAC	
211	Gly	Arg	Val	Thr	Arg	Gly	Ser	Glu	Arg	Phe	Arg	Asp	Leu	Val	Pro	Asn	
212	65					70					75				80		288
214	TAC	AAC	CCC	GAC	ATA	AIC	TTC	AAG	GAT	GAG	GAG	AAC	AGC	GGC	GCA	GAC	
215	Tyr	Asn	Pro	Asp	Ile	Ile	Phe	Lys	Asp	Glu	Glu	Asn	Ser	Gly	Ala	Asp	
216					85					90				95			336
218	CGC	CTG	ATG	ACA	GAG	CGT	PGC	AAA	GAG	CGG	GTG	AAC	GCT	CTA	GCC	ATC	
219	Arg	Leu	Met	Thr	Glu	Arg	Cys	Lys	Glu	Arg	Val	Asn	Ala	Leu	Ala	Ile	
220				100				105					110				384
222	GCG	GTG	ATG	AAC	ATG	TGG	CCC	GGA	GTA	CGC	CTA	CGT	GTG	ACT	GAA	GGC	
223	Ala	Val	Met	Asn	Met	Trp	Pro	Gly	Val	Arg	Leu	Arg	Val	Thr	Glu	Gly	
224		115						120			125						432
226	TGG	GAC	GAG	GAC	GGC	CAC	CAC	GCA	CAG	GAT	TCA	CTC	CAC	TAC	GAA	GGC	
227	Trp	Asp	Glu	Asp	Gly	His	His	Ala	Gln	Asp	Ser	Leu	His	Tyr	Glu	Gly	
228		130				135					140						480
230	CGT	GCC	TTG	GAC	ATC	ACC	ACG	TCT	GAC	CGT	GAC	CGT	AAT	AAG	TAT	GGT	
231	Arg	Ala	Leu	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Arg	Asn	Lys	Tyr	Gly	
232	145				150					155				160			528
234	TTG	TTG	GCG	CGC	CTA	GCT	GTG	GAA	GCC	GGA	TTC	GAC	TGG	GTC	TAC	TAC	
235	Leu	Leu	Ala	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	Tyr	Tyr	
236			165					170					175				576
238	GAG	TCC	CGC	AAC	CAC	ATC	CAC	GTA	TCG	GTC	AAA	GCT	GAT	AAC	TCA	CTG	
239	Glu	Ser	Arg	Asn	His	Ile	His	Val	Ser	Val	Lys	Ala	Asp	Asn	Ser	Leu	
240			180					185				190					624
242	GCG	GTC	CGA	GCC	GGA	GGC	TGC	TTT	CCG	GGA	AAT	GCC	ACG	GTG	CGC	TTC	
243	Ala	Val	Arg	Ala	Gly	Gly	Cys	Phe	Pro	Gly	Asn	Ala	Thr	Val	Arg	Leu	
244			195				200				205						672
246	CGG	AGC	GGC	GAA	CGG	AAG	GGG	CTG	AGG	GAA	CTA	CAT	CGT	GGT	GAC	TGG	
247	Arg	Ser	Gly	Glu	Arg	Lys	Gly	Leu	Arg	Glu	Leu	His	Arg	Gly	Asp	Trp	
248		210				215					220						720
250	GTA	CTG	GCC	GCT	GAT	GCA	GCG	GGC	CGA	GTG	GTA	CCC	ACG	CCA	GTG	CTG	
251	Val	Leu	Ala	Ala	Asp	Ala	Ala	Gly	Arg	Val	Val	Pro	Thr	Pro	Val	Leu	
252	225					230					235						768
254	CTC	TTC	CTG	GAC	CGG	GAT	CTG	CAG	CGC	CGC	TCG	TTC	GTG	GCT	GTG		
255	Leu	Phe	Leu	Asp	Arg	Asp	Leu	Gln	Arg	Arg	Ala	Ser	Phe	Val	Ala	Val	
256				245						250				255			816
258	GAG	ACC	GAG	CGG	CCT	CCG	CGC	AAA	CTG	TTG	CTC	ACA	CCC	TGG	CAT	CTG	
259	Glu	Thr	Glu	Arg	Pro	Pro	Arg	Lys	Leu	Leu	Leu	Thr	Pro	Trp	His	Leu	
260			260					265					270				864
262	GTG	TTC	GCT	GCT	CGC	GGG	CCA	GCG	CCT	GCT	CCA	GGT	GAC	TTT	GCA	CCG	
263	Val	Phe	Ala	Ala	Arg	Gly	Pro	Ala	Pro	Ala	Pro	Gly	Asp	Phe	Ala	Pro	
264			275				280						285				912
266	GTG	TTC	GCG	CGC	CGC	TTA	CGT	GCT	GGC	GAC	TCG	GTG	CTG	GCT	CCC	GGC	
267	Val	Phe	Ala	Arg	Arg	Leu	Arg	Ala	Gly	Asp	Ser	Val	Leu	Ala	Pro	Gly	

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268      290      295      300
270 GGG GAC GCG CTC CAG CCG GCG CGC GTA GCC CGC GTG GCG CGC GAG GAA      960
271 Gly Asp Ala Leu Gln Pro Ala Arg Val Ala Arg Val Ala Arg Glu Glu
272 305      310      315      320
274 GCC GTG GGC GTG TTC GCA CCG CTC ACF GCG CAC GGG ACG CTG CTG GIC      1008
275 Ala Val Gly Val Phe Ala Pro Leu Thr Ala His Gly Thr Leu Leu Val
276      325      330      335
278 AAC GAC GTC CTC GCC TCC TGC TAC GCG GTT CTA GAG AGT CAC CAG TGG      1056
279 Asn Asp Val Leu Ala Ser Cys Tyr Ala Val Leu Glu Ser His Gln Trp
280      340      345      350
282 GCC CAC CGC GCC TTC GCC CCT TTG CGG CTG CTG CAC GCG CTC GGG GCT      1104
283 Ala His Arg Ala Phe Ala Pro Leu Arg Leu Leu His Ala Leu Gly Ala
284      355      360      365
286 CTG CTC CCI GGG GGT GCA GTC CAG CCG ACT GGC ATG CAT TGG TAC TCT      1152
287 Leu Leu Pro Gly Gly Ala Val Gln Pro Thr Gly Met His Trp Tyr Ser
288      370      375      380
290 CGC CTC CTT TAC CGC TTG GCC GAG GAG TTA ATG GGC TG      1190
291 Arg Leu Leu Tyr Arg Leu Ala Glu Glu Leu Met Gly
292 385      390      395
295 (2) INFORMATION FOR SEQ ID NO: 3:
297 (i) SEQUENCE CHARACTERISTICS:
298 (A) LENGTH: 1056 base pairs
299 (B) TYPE: nucleic acid
300 (C) STRANDEDNESS: both
301 (D) TOPOLOGY: linear
303 (ii) MOLECULE TYPE: cDNA
306 (ix) FEATURE:
307 (A) NAME/KEY: CDS
308 (B) LOCATION: 1..1008
311 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
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314 Glu Arg Phe Lys Glu Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile Phe
315 1      5      10      15
317 AAG GAC GAG GAG AAC ACG GGT GCC GAC CGC CTC ATG ACC CAG CGC TGC      96
318 Lys Asp Glu Glu Asn Thr Gly Ala Asp Arg Leu Met Thr Gln Arg Cys
319      20      25      30
321 AAG GAC CGT CTG AAC TCA CTG GCC ATC TCT GTC ATG AAC CAG TGG CCT      144
322 Lys Asp Arg Leu Asn Ser Leu Ala Ile Ser Val Met Asn Gln Trp Pro
323      35      40      45
325 GGT GTG AAA CTG CGG GTG ACC GAA GGC CGG GAT GAA GAT GGC CAT CAC      192
326 Gly Val Lys Leu Arg Val Thr Glu Gly Arg Asp Glu Asp Gly His His
327      50      55      60
329 TCA GAG GAG TCT TTA CAC TAT GAG GGC CGC GCG GTG GAT ATC ACC ACC      240
330 Ser Glu Glu Ser Leu His Tyr Glu Gly Arg Ala Val Asp Ile Thr Thr
331      65      70      75      80
333 TCA GAC CGT GAC CGA AAT AAG TAT GGA CTG CTG GCG CGC TTA GCA GTG      288
334 Ser Asp Arg Asp Arg Asn Lys Tyr Gly Leu Leu Ala Arg Leu Ala Val
335      85      90      95
337 GAG GCC GGC TTC GAC TGG GTG TAT TAC GAG TCC AAG GCC CAC GTG CAT      336

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L:31 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:32 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:789 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:1434 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:2148 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40
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